

INPUT SET: S1134.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Inouye, Sumiko
Hsu, Mei-Yin
Eagle, Susan
Inouye, Masayori

10 (ii) TITLE OF INVENTION: Prokaryotic Reverse Transcriptase

12 (iii) NUMBER OF SEQUENCES: 42

14 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Weiser

- (B) STREET: 230 South Fifteenth Street, Suite 500
- (C) CITY: Philadelphia
- (D) STATE: Pennsylvania
- (E) COUNTRY: U.S.A.
- (F) ZIP: 19102

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/269,118
(B) FILING DATE: 10-JUN-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Weiser, Gerard J.
(B) REGISTRATION NUMBER: 19,763
(C) REFERENCE/DOCKET NUMBER: 377-5888P

(ix) TELECOMMUNICATION INFORMATION.

(A) TELEPHONE: 215-875-8383
(B) TELEFAX: 215-875-8394

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2176 base pairs

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47 (B) TYPE: nucleic acid
 48 (C) STRANDEDNESS: double
 49 (D) TOPOLOGY: linear
 50
 51
 52 (ix) FEATURE:
 53 (A) NAME/KEY: CDS
 54 (B) LOCATION: 640..2094
 55
 56
 57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 58
 59 TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG 60
 60
 61 TGTACCGCGT TTCCCTGGAT GGTACACCTGG TGGCGGTGGA GTGGGGCCCG CGCACGGGCT 120
 62
 63 CGCCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG 180
 64
 65 CGCGCCTCGA GAAAGTTGGCG GCTGACGGCT ACATCGACGC GCCCTCGGCA TTGGTCTAAA 240
 66
 67 CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG 300
 68
 69 ACGACGTGCG CTTCACGCGC GAGCAGCCGA GAGAGGTCCG GAGTGCATCA GCCTGAGCGC 360
 70
 71 CTCGAGCGGC GGAGCGCGT TGCGCCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG 420
 72
 73 TAGCCTGTT TC TGCGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGTA GCGGAGCAA 480
 74
 75 CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG 540
 76
 77 CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT 600
 78
 79 GTCCCGTCTT CCATCGCCGC GCCCGCCCAA GGTGCAGAC ATG ACC GCC AGG CTG 654
 80 Met Thr Ala Arg Leu
 81 1 5
 82
 83 GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG 702
 84 Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu
 85 10 15 20
 86
 87 CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG 750
 88 Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg Glu Ala Arg Arg
 89 25 30 35
 90
 91 CTC GCG CAC GAA GCG TTG CTC GTC CGC GCG AAG GCC ATC GAC GAA GCG 798
 92 Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala
 93 40 45 50
 94
 95 GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC 846
 96 Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu
 97 55 60 65
 98
 99 GCG GTC GAG GAC CTG GAC TTC TCC AGC GCC TCC GAG AAG GAC AAG AAG 894

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100	Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu Lys Asp Lys Lys			
101	70	75	80	85
102				
103	GCC TGG AAG GAG AAG AAG GCC GAG GCC ACC GAG CGC CGC GCG CTG			942
104	Ala Trp Lys Glu Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Leu			
105	90	95	100	
106				
107	AAG CGT CAG GCG CAC GAG GCG TGG AAG GCC ACG CAC GTG GGC CAC CTG			990
108	Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His Val Gly His Leu			
109	105	110	115	
110				
111	GGC GCG GGC GTG CAC TGG GCG GAG GAC CGC CTG GCC GAC GCG TTC GAC			1038
112	Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu Ala Asp Ala Phe Asp			
113	120	125	130	
114				
115	GTG CCC CAC CGC GAG GAG CGC GCC CGG GCC AAC GGC CTG ACG GAG CTG			1086
116	Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn Gly Leu Thr Glu Leu			
117	135	140	145	
118				
119	GAC TCC GCG GAG GCG CTG GCC AAG GCG CTG GGG CTG AGC GTC TCC AAG			1134
120	Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly Leu Ser Val Ser Lys			
121	150	155	160	165
122				
123	CTC CGC TGG TTC GCG TTC CAC CGG GAG GTC GAC ACG GCC ACG CAC TAC			1182
124	Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr			
125	170	175	180	
126				
127	GTG AGC TGG ACC ATT CCG AAG CGG GAC GGC AGC AAG CGC ACG ATT ACG			1230
128	Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr			
129	185	190	195	
130				
131	TCC CCC AAG CCT GAG CTG AAG GCA GCG CAG CGC TGG GTG CTG TCC AAC			1278
132	Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn			
133	200	205	210	
134				
135	GTC GTG GAG CGG CTG CCG GTC CAC GGC GCC CAC GGC TTC GTG GCG			1326
136	Val Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala			
137	215	220	225	
138				
139	GGA CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTC			1374
140	Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val			
141	230	235	240	245
142				
143	GTG GTC AAG GTG GAC CTC AAG GAC TTC TTC CCC TCC GTC ACC TGG CGC			1422
144	Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg			
145	250	255	260	
146				
147	CGG GTG AAG GGC CTG TTG CGC AAG GGC GGC CTG CGG GAG GGC ACG TCC			1470
148	Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser			
149	265	270	275	
150				
151	ACG CTG CTG TCC CTC CTC TCC ACG GAA GCG CCG CGG GAG GCG GTC CAG			1518
152	Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln			

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153	280	285	290	
154				
155	TTC CGC GGC AAG CTC CTG CAC GTC GCC AAG GGC CCG CGC GCC CTG CCC			1566
156	Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro			
157	295	300	305	
158				
159	CAG GGC GCC CCC ACG TCG CCC GGC ATC ACC AAC GCG CTC TGC CTG AAG			1614
160	Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys			
161	310	315	320	325
162				
163	CTC GAC AAG CGG CTG TCC GCC CTC GCG AAG CGG CTG GGC TTC ACC TAC			1662
164	Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr			
165	330	335	340	
166				
167	ACG CGC TAC GCG GAC GAC CTG ACC TTC TCC TGG ACG AAG GCG AAG CAG			1710
168	Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln			
169	345	350	355	
170				
171	CCC AAG CCG CGG CGG ACG CAG CGT CCC CCC GTC GCG GTC CTC CTG TCT			1758
172	Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser			
173	360	365	370	
174				
175	CGC GTC CAG GAA GTG GTG GAG GCG GAG GGC TTC CGC GTG CAC CCG GAC			1806
176	Arg Val Gln Glu Val Val Ala Glu Gly Phe Arg Val His Pro Asp			
177	375	380	385	
178				
179	AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC			1854
180	Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu			
181	390	395	400	405
182				
183	GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC			1902
184	Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg			
185	410	415	420	
186				
187	GAC GTC GTC CGC CAG CTC CGC GCC GCC ATC CAC AAC CGG AAG AAG GGC			1950
188	Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly			
189	425	430	435	
190				
191	AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC			1998
192	Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala			
193	440	445	450	
194				
195	GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT			2046
196	Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala			
197	455	460	465	
198				
199	CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG			2094
200	Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu			
201	470	475	480	485
202				
203	TGACCGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCGCGCC AGCAACGCCG CATTCAAGCAA			2154
204				
205	CTCCGTCAGC CGGCGCGGGT AC			2176

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207

208 (2) INFORMATION FOR SEQ ID NO:2:

209

210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 263 amino acids
212 (B) TYPE: amino acid
213 (D) TOPOLOGY: linear

214

215 (ii) MOLECULE TYPE: protein

216

217

218

219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

220

221 Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro
222 1 5 10 15

223

224 Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met
225 20 25 30

226

227 Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn
228 35 40 45

229

230 Thr Pro Val Phe Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys
231 50 55 60

232

233 Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu
234 65 70 75 80

235

236 Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser
237 85 90 95

238

239 Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp
240 100 105 110

241

242 Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
243 115 120 125

244

245 Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp
246 130 135 140

247

248 Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu
249 145 150 155 160

250

251 Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
252 165 170 175

253

254 Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys
255 180 185 190

256

257 Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro
258 195 200 205

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SEQUENCE VERIFICATION REPORT
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